

## **AMENDMENTS TO THE CLAIMS:**

The listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-11 (Cancelled)

12. (Previously amended): A method of high throughput integrated genomics comprising:
- a) providing a plurality of enhanced homologous recombination (EHR) compositions, wherein each composition comprises:
    - i) a recombinase;
    - ii) a first and a second targeting polynucleotide, wherein said first targeting polynucleotide comprises a portion substantially complementary to a fragment of a target nucleic acid and is substantially complementary to said second targeting polynucleotide; and
    - iii) a separation moiety;
  - b) contacting said EHR compositions with a library of target nucleic acid(s) under conditions wherein said targeting polynucleotides hybridize to one or more target nucleic acids of said library; and
  - c) isolating and cloning said target nucleic acid(s) wherein said isolating and cloning are performed using a robotic system.
13. (Previously amended): The method according to claim 12, wherein said target nucleic acid is a target gene.
14. (Previously amended): The method according to claim 13, wherein said target nucleic acid is a portion of said target gene.
15. (Previously amended): The method according to claim 12, wherein said target nucleic acid is a regulatory sequence.
16. (Previously amended): The method according to claim 12, wherein said target nucleic acid comprises single-polynucleotide polymorphisms.

17. (Previously amended): The method according to claim 12, wherein said library of target nucleic acids comprises all or part of a cDNA library, genomic DNA library, genomic DNA samples, or combinations thereof.
18. (Previously amended): The method of claim 17, wherein said genomic DNA samples are from one or more organisms.
19. (Previously amended): The method according to claim 12 further comprising:
- d) making a library of nucleic acid variants of said target nucleic acid;
  - e) introducing said library of nucleic acid variants into a cellular library; and
  - f) performing phenotypic screening on said cellular library.
20. (Previously amended): The method according to claim 19 wherein at least one of said making, introducing and performing steps is performed using a robotic system.
21. (Previously amended): The method according to claim 12 further comprising:
- d) making a plurality of cells comprising a mutant target nucleic acid;
  - e) adding a library of candidate agents to said plurality; and
  - f) determining the effect of said candidate agents on said cells.
22. (Previously amended): The method according to claim 21 wherein at least one of said making, adding, and determining steps is performed using a robotic system.
23. (Previously amended): The method according to claim 21, wherein said mutant target nucleic acid is a gene sequence knock-out or a gene sequence knock-in.
24. (Previously amended): The method according to claim 21, wherein said mutant target nucleic acid comprises an insertion, substitution, deletion or combinations thereof.

Claims 25-27 (Cancelled)

28. (Previously amended): The method according to claim 12 further comprising sequencing said target nucleic acid.

Claims 29-32 (Cancelled)

33. (Previously amended): The method of claim 12, wherein said robotic system comprises a computer workstation comprising a microprocessor programmed to manipulate a device selected from the group consisting of a thermocycler, a multichannel pipettor, a sample handler, a plate handler, a gel loading system, a gene sequencer, an automated transformation system, a colony picker, a bead picker, a cell sorter, an incubator, a light microscope, a fluorescence microscope, a spectrofluorimeter, a spectrophotometer, a luminometer, a CCD camera and combinations thereof.

Claims 34-48 (Cancelled)

49. (Previously amended): The method of claim 17, wherein said genomic library comprises nucleic acid from a combination of multiple organisms.

Claims 50-51 (Cancelled)